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 TECH CENTER 1600/2900

C 54 to 74	hPL (56-64) pGH (57-73)	E56D, R64M S57T, T60A, S62T, N63G, R64K, E65D, T67A, K70R, N72D, L73V	Cassette Cassette	10 5.8	30 17
	hPRL (54-74)	F54H, S55T, E56S, I58L, P59A, S62E, N63D, R64K, E66Q, T67A, K70M, S71N, N72Q, L73K, E74D	Cassette	23	69
D 88 to 104	hPRL (88-95)	E88G, Q91Y, F92H, R94T, S95E	RS	0.47	1.4
	hPRL (97-104)	F97R, A98G, N99M, S100Q, L101D, V102A, Y103P, G104E	RS	0.53	1.6
E 108 to 136	hPL (109-112) hPRL (111-129)	N109D, V110D, D112H Y111V, L113I, K115E, D116Q, E118K, E119R, G120L, Q122E, T123G, G126L, R127I, E129S	Cassette Cassette	0.61 0.52	1.8 1.5
	hPRL (126-136)	R127D, L128V, E129H, D130P, G131E, S132T, P133K, R134E, T135N	Cassette	0.58	1.7
F164 to 190	pGH (164-190)	Y164S, R167K, M170L, D171H, V173A, F176Y, I179V, V180M, Q181K, S184R, I184F, G187S, G190A	Hybrid	≥34	≥100
	pGH (167-181)	R167K, D171H, I179V, Q181K	RS	9.2	27

The dissociation constants (K_D) were calculated from Scatchard analysis of competitive binding of 125 labeled hGH to the cloned and purified soluble hGH receptor at 25°C (23). Standard errors in these measurements were generally at or below ±20 percent. Mutants are named on the basis of the first and last residue mutated in the region. The specific mutations introduced are described by a nomenclature where the wild-type hGH residue is given first followed by its sequence position and then the mutant residue. The single letter code designates each amino acid.--

Format page 17, lines 1-2 so "A comparison" begins a new paragraph.

At page 17, line 16, insert,

--The complete results are given in the table below:

Table B: Binding of Alanine Substitution (Residues 2-19, 54-74, and 167-191) Mutants of hGH to the soluble hGH receptor.

Mutant	K _d (nM)	Mutant	K _d (nM)
wt	0.34	Q69A	0.31
P2A	0.31	K70A	0.82
T3A	0.31	S71A	0.68
I4A	0.68	N72A	NE
P5A	0.71	L73A	0.24
L6A	0.95	E74A	NE
S7A	0.61		
R8A	0.48	R167A	0.26
L9A	0.32	K168A	0.37
F10A	2.0	D169A	NE
D11A	NE	M170A	NE
N12A	0.40	D171A	2.4
A13(wt)		K172A	4.6
M14A	0.75	V173A	NE
L15A	0.44	E174A	0.075
R16A	0.51	T175A	NE
A17(wt)		T175S	5.9
H18A	0.24	F176A	5.4
R19A	0.37	L177A	NE
		R178A	NE
F54A	1.5	R178N	2.9
S55A	0.41	I179A	0.92
E56A	1.4	V180A	0.34
S57A	0.48	Q181A	0.54
I58A	5.6	C182A	1.9
P59A	0.65	R183A	0.71
T60A	NE	S184A	0.31
P61A	NE	V185A	1.5
S62A	0.95	E186A	0.27
N63A	1.12	G187A	0.61
R64A	7.11	S188A	0.24
E65A	0.20	C189A	NE
E66A	0.71	G190A	NE
T67A	NE	F191A	0.47
Q68A	1.8		

NE ("not expressed") indicates the mutant protein was expressed below 2% of wild-type hGH as determined by SDS-PAGE or ELISA.--

IN THE CLAIMS